RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: _10/773,455A_
Source: _/FWO_
Date Processed by STIC: _10/16/06_

ENTERED

IFWO

RAW SEQUENCE LISTING   DATE: 10/16/2006
PATENT APPLICATION: US/10/773,455A   TIME: 11:40:00

Input Set : **A:\08919-111001.txt**
Output Set: **N:\CRF4\10162006\J773455A.raw**

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 4 <110> APPLICANT: Shyur, Lie-Fen
 5         Wen, Tuan-Nan
 6         Lee, Shu-Hua
 7         Yang, Ning-Sun
 9 <120> TITLE OF INVENTION: Truncated 1,3-1,4-Beta-D-Glucanase
12 <130> FILE REFERENCE: 08919-111001
14 <140> CURRENT APPLICATION NUMBER: US 10/773,455A
15 <141> CURRENT FILING DATE: 2004-02-06
17 <150> PRIOR APPLICATION NUMBER: US 09/654,652
18 <151> PRIOR FILING DATE: 2000-09-05
20 <160> NUMBER OF SEQ ID NOS: 22
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 349
26 <212> TYPE: PRT
27 <213> ORGANISM: Fibrobacter succinogenes
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32 Ala Ala Ala Ala Leu Thr Thr Asn Val Ser Ala Lys Asp Phe Ser Gly
33             20                  25                  30
34 Ala Glu Leu Tyr Thr Leu Glu Glu Val Gln Tyr Gly Lys Phe Glu Ala
35         35                  40                  45
36 Arg Met Lys Met Ala Ala Ala Ser Gly Thr Val Ser Ser Met Phe Leu
37     50                  55                  60
38 Tyr Gln Asn Gly Ser Glu Ile Ala Asp Gly Arg Pro Trp Val Glu Val
39 65                  70                  75                  80
40 Asp Ile Glu Val Leu Gly Lys Asn Pro Gly Ser Phe Gln Ser Asn Ile
41                 85                  90                  95
42 Ile Thr Gly Lys Ala Gly Ala Gln Lys Thr Ser Glu Lys His His Ala
43                 100                 105                 110
44 Val Ser Pro Ala Ala Asp Gln Ala Phe His Thr Tyr Gly Leu Glu Trp
45         115                 120                 125
46 Thr Pro Asn Tyr Val Arg Trp Thr Val Asp Gly Gln Glu Val Arg Lys
47     130                 135                 140
48 Thr Glu Gly Gly Gln Val Ser Asn Leu Thr Gly Thr Gln Gly Leu Arg
49 145                 150                 155                 160
50 Phe Asn Leu Trp Ser Ser Glu Ser Ala Ala Trp Val Gly Gln Phe Asp
51                 165                 170                 175
52 Glu Ser Lys Leu Pro Leu Phe Gln Phe Ile Asn Trp Val Lys Val Tyr
53             180                 185                 190
54 Lys Tyr Thr Pro Gly Gln Gly Glu Gly Gly Ser Asp Phe Thr Leu Asp
55     195                 200                 205
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56 Trp Thr Asp Asn Phe Asp Thr Phe Asp Gly Ser Arg Trp Gly Lys Gly
57     210                 215                 220
58 Asp Trp Thr Phe Asp Gly Asn Arg Val Asp Leu Thr Asp Lys Asn Ile
59 225                 230                 235                 240
60 Tyr Ser Arg Asp Gly Met Leu Ile Leu Ala Leu Thr Arg Lys Gly Gln
61                 245                 250                 255
62 Glu Ser Phe Asn Gly Gln Val Pro Arg Asp Asp Glu Pro Ala Pro Gln
63                 260                 265                 270
64 Ser Ser Ser Ser Ala Pro Ala Ser Ser Ser Ser Val Pro Ala Ser Ser
65             275                 280                 285
66 Ser Ser Val Pro Ala Ser Ser Ser Ser Ala Phe Val Pro Pro Ser Ser
67     290                 295                 300
68 Ser Ser Ala Thr Asn Ala Ile His Gly Met Arg Thr Thr Pro Ala Val
69 305                 310                 315                 320
70 Ala Lys Glu His Arg Asn Leu Val Asn Ala Lys Gly Ala Lys Val Asn
71                 325                 330                 335
72 Pro Asn Gly His Lys Arg Tyr Arg Val Asn Phe Glu His
73                 340                 345
76 <210> SEQ ID NO: 2
77 <211> LENGTH: 27
78 <212> TYPE: PRT
79 <213> ORGANISM: Fibrobacter succinogenes
81 <400> SEQUENCE: 2
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84 Ala Ala Ala Ala Leu Thr Thr Asn Val Ser Ala
85             20                  25
88 <210> SEQ ID NO: 3
89 <211> LENGTH: 175
90 <212> TYPE: PRT
91 <213> ORGANISM: Fibrobacter succinogenes
93 <400> SEQUENCE: 3
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95 1               5                   10                  15
96 Gly Lys Phe Glu Ala Arg Met Lys Met Ala Ala Ala Ser Gly Thr Val
97             20                  25                  30
98 Ser Ser Met Phe Leu Tyr Gln Asn Gly Ser Glu Ile Ala Asp Gly Arg
99         35                  40                  45
100 Pro Trp Val Glu Val Asp Ile Glu Val Leu Gly Lys Asn Pro Gly Ser
101     50                  55                  60
102 Phe Gln Ser Asn Ile Ile Thr Gly Lys Ala Gly Ala Gln Lys Thr Ser
103 65                  70                  75                  80
104 Glu Lys His His Ala Val Ser Pro Ala Ala Asp Gln Ala Phe His Thr
105                 85                  90                  95
106 Tyr Gly Leu Glu Trp Thr Pro Asn Tyr Val Arg Trp Thr Val Asp Gly
107             100                 105                 110
108 Gln Glu Val Arg Lys Thr Glu Gly Gly Gln Val Ser Asn Leu Thr Gly
109         115                 120                 125
110 Thr Gln Gly Leu Arg Phe Asn Leu Trp Ser Ser Glu Ser Ala Ala Trp
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                  RAW SEQUENCE LISTING              DATE: 10/16/2006
                  PATENT APPLICATION:   US/10/773,455A    TIME: 11:40:00

                  Input Set : A:\08919-111001.txt
                  Output Set: N:\CRF4\10162006\J773455A.raw
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111      130                    135                    140
112 Val Gly Gln Phe Asp Glu Ser Lys Leu Pro Leu Phe Gln Phe Ile Asn
113 145                    150                    155                    160
114 Trp Val Lys Val Tyr Lys Tyr Thr Pro Gly Gln Gly Glu Gly Gly
115                    165                    170                    175
118 <210> SEQ ID NO: 4
119 <211> LENGTH: 64
120 <212> TYPE: PRT
121 <213> ORGANISM: Fibrobacter succinogenes
123 <400> SEQUENCE: 4
124 Ser Asp Phe Thr Leu Asp Trp Thr Asp Asn Phe Asp Thr Phe Asp Gly
125 1                    5                    10                    15
126 Ser Arg Trp Gly Lys Gly Asp Trp Thr Phe Asp Gly Asn Arg Val Asp
127             20                    25                    30
128 Leu Thr Asp Lys Asn Ile Tyr Ser Arg Asp Gly Met Leu Ile Leu Ala
129         35                    40                    45
130 Leu Thr Arg Lys Gly Gln Glu Ser Phe Asn Gly Gln Val Pro Arg Asp
131     50                    55                    60
134 <210> SEQ ID NO: 5
135 <211> LENGTH: 78
136 <212> TYPE: PRT
137 <213> ORGANISM: Fibrobacter succinogenes
139 <400> SEQUENCE: 5
140 Gln Ser Ser Ser Ser Ala Pro Ala Ser Ser Ser Ser Val Pro Ala Ser
141 1                    5                    10                    15
142 Ser Ser Ser Val Pro Ala Ser Ser Ser Ser Ala Phe Val Pro Pro Ser
143             20                    25                    30
144 Ser Ser Ser Ala Thr Asn Ala Ile His Gly Met Arg Thr Thr Pro Ala
145         35                    40                    45
146 Val Ala Lys Glu His Arg Asn Leu Val Asn Ala Lys Gly Ala Lys Val
147     50                    55                    60
148 Asn Pro Asn Gly His Lys Arg Tyr Arg Val Asn Phe Glu His
149 65                    70                    75
152 <210> SEQ ID NO: 6
153 <211> LENGTH: 1050
154 <212> TYPE: DNA
155 <213> ORGANISM: Fibrobacter succinogenes
157 <220> FEATURE:
158 <221> NAME/KEY: CDS
159 <222> LOCATION: (1)...(1047)
161 <400> SEQUENCE: 6
162 atg aac atc aag aaa act gca gtc aag agc gct ctc gcc gta gca gcc    48
163 Met Asn Ile Lys Lys Thr Ala Val Lys Ser Ala Leu Ala Val Ala Ala
164 1                    5                    10                    15
166 gca gca gca gcc ctc acc acc aat gtt agc gca aag gat ttt agc ggt    96
167 Ala Ala Ala Ala Leu Thr Thr Asn Val Ser Ala Lys Asp Phe Ser Gly
168             20                    25                    30
170 gcc gaa ctc tac acg tta gaa gaa gtt cag tac ggt aag ttt gaa gcc   144
171 Ala Glu Leu Tyr Thr Leu Glu Glu Val Gln Tyr Gly Lys Phe Glu Ala
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172          35                    40                    45
174 cgt atg aag atg gca gcc gca tcg gga aca gtc agt tcc atg ttc ctc   192
175 Arg Met Lys Met Ala Ala Ala Ser Gly Thr Val Ser Ser Met Phe Leu
176          50                    55                    60
178 tac cag aat ggt tcc gaa atc gcc gat gga agg ccc tgg gta gaa gtg   240
179 Tyr Gln Asn Gly Ser Glu Ile Ala Asp Gly Arg Pro Trp Val Glu Val
180  65                    70                    75                    80
182 gat att gaa gtt ctc ggc aag aat ccg ggc agt ttc cag tcc aac atc   288
183 Asp Ile Glu Val Leu Gly Lys Asn Pro Gly Ser Phe Gln Ser Asn Ile
184                    85                    90                    95
186 att acc ggt aag gcc ggc gca caa aag act agc gaa aag cac cat gct   336
187 Ile Thr Gly Lys Ala Gly Ala Gln Lys Thr Ser Glu Lys His His Ala
188          100                   105                   110
190 gtt agc ccc gcc gcc gat cag gct ttc cac acc tac ggt ctc gaa tgg   384
191 Val Ser Pro Ala Ala Asp Gln Ala Phe His Thr Tyr Gly Leu Glu Trp
192          115                   120                   125
194 act ccg aat tac gtc cgc tgg act gtt gac ggt cag gaa gtc cgc aag   432
195 Thr Pro Asn Tyr Val Arg Trp Thr Val Asp Gly Gln Glu Val Arg Lys
196          130                   135                   140
198 acg gaa ggt ggc cag gtt tcc aac ttg aca ggt aca cag gga ctc cgt   480
199 Thr Glu Gly Gly Gln Val Ser Asn Leu Thr Gly Thr Gln Gly Leu Arg
200 145                   150                   155                   160
202 ttt aac ctt tgg tcg tct gag agt gcg gct tgg gtt ggc cag ttc gat   528
203 Phe Asn Leu Trp Ser Ser Glu Ser Ala Ala Trp Val Gly Gln Phe Asp
204                    165                   170                   175
206 gaa tca aag ctt ccg ctt ttc cag ttc atc aac tgg gtc aag gtt tat   576
207 Glu Ser Lys Leu Pro Leu Phe Gln Phe Ile Asn Trp Val Lys Val Tyr
208          180                   185                   190
210 aag tat acg ccg ggc cag ggc gaa ggc ggc agc gac ttt acg ctt gac   624
211 Lys Tyr Thr Pro Gly Gln Gly Glu Gly Gly Ser Asp Phe Thr Leu Asp
212          195                   200                   205
214 tgg acc gac aat ttt gac acg ttt gat ggc tcc cgc tgg ggc aag ggt   672
215 Trp Thr Asp Asn Phe Asp Thr Phe Asp Gly Ser Arg Trp Gly Lys Gly
216          210                   215                   220
218 gac tgg aca ttt gac ggt aac cgt gtc gac ctc acc gac aag aac atc   720
219 Asp Trp Thr Phe Asp Gly Asn Arg Val Asp Leu Thr Asp Lys Asn Ile
220 225                   230                   235                   240
222 tac tcc aga gat ggc atg ttg atc ctc gcc ctc acc cgc aaa ggt cag   768
223 Tyr Ser Arg Asp Gly Met Leu Ile Leu Ala Leu Thr Arg Lys Gly Gln
224          245                   250                   255
226 gaa agc ttc aac ggc cag gtt ccg aga gat gac gaa cct gct ccg caa   816
227 Glu Ser Phe Asn Gly Gln Val Pro Arg Asp Asp Glu Pro Ala Pro Gln
228          260                   265                   270
230 tct tct agc agc gct ccg gca tct tct agc agt gtt ccg gca agc tcc   864
231 Ser Ser Ser Ser Ala Pro Ala Ser Ser Ser Ser Val Pro Ala Ser Ser
232          275                   280                   285
234 tct agc gtc cct gcc tcc tcg agc agc gca ttt gtt ccg ccg agc tcc   912
235 Ser Ser Val Pro Ala Ser Ser Ser Ser Ala Phe Val Pro Pro Ser Ser
236          290                   295                   300
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238 tcg agc gcc aca aac gca atc cac gga atg cgc aca act ccg gca gtt   ·960
239 Ser Ser Ala Thr Asn Ala Ile His Gly Met Arg Thr Thr Pro Ala Val
240 305               310               315               320
242 gca aag gaa cac cgc aat ctc gtg aac gcc aag ggt gcc aag gtg aac   1008
243 Ala Lys Glu His Arg Asn Leu Val Asn Ala Lys Gly Ala Lys Val Asn
244               325               330               335
246 ccg aat ggc cac aag cgt tat cgc gtg aac ttt gaa cac taa           1050
247 Pro Asn Gly His Lys Arg Tyr Arg Val Asn Phe Glu His
248               340               345
251 <210> SEQ ID NO: 7
252 <211> LENGTH: 248
·253 <212> TYPE: PRT
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
257 <223> OTHER INFORMATION: Synthetic construct
259 <400> SEQUENCE: 7
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261 1               5               10               15
262 Glu Val Gln Tyr Gly Lys Phe Glu Ala Arg Met Lys Met Ala, Ala Ala
263               20               25               30
264 Ser Gly Thr Val Ser Ser Met Phe Leu Tyr Gln Asn Gly Ser Glu Ile
265               35               40               45
266 Ala Asp Gly Arg Pro Trp Val Glu Val Asp Ile Glu Val Leu Gly Lys
267       50               55               60
268 Asn Pro Gly Ser Phe Gln Ser Asn Ile Ile Thr Gly Lys Ala Gly Ala
269 65               70               75               80
270 Gln Lys Thr Ser Glu Lys His His Ala Val Ser Pro Ala Ala Asp Gln
271               85               90               95
272 Ala Phe His Thr Tyr Gly Leu Glu Trp Thr Pro Asn Tyr Val Arg Trp
273               100               105               110
274 Thr Val Asp Gly Gln Glu Val Arg Lys Thr Glu Gly Gly Gln Val Ser
275               115               120               125
276 Asn Leu Thr Gly Thr Gln Gly Leu Arg Phe Asn Leu Trp Ser Ser Glu
277       130               135               140
278 Ser Ala Ala Trp Val Gly Gln Phe Asp Glu Ser Lys Leu Pro Leu Phe
279 145               150               155               160
280 Gln Phe Ile Asn Trp Val Lys Val Tyr Lys Tyr Thr Pro Gly Gln Gly
281               165               170               175
282 Glu Gly Gly Ser Asp Phe Thr Leu Asp Trp Thr Asp Asn Phe Asp Thr
283               180               185               190
284 Phe Asp Gly Ser Arg Trp Gly Lys Gly Asp Trp Thr Phe Asp Gly Asn
285       195               200               205
286 Arg Val Asp Leu Thr Asp Lys Asn Ile Tyr Ser Arg Asp Gly Met Leu
287       210               215               220
288 Ile Leu Ala Leu Thr Arg Lys Gly Gln Glu Ser Phe Asn Gly Gln Val
289 225               230               235               240
290 Pro Arg Asp Asp Glu Pro Ala Pro
291               245
294 <210> SEQ ID NO: 8
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/773,455A**

DATE: 10/16/2006
TIME: 11:40:01

Input Set : **A:\08919-111001.txt**
Output Set: **N:\CRF4\10162006\J773455A.raw**